



# 5

- 1 -

## SEQUENCE LISTING

<110> Ford et al.

<120> EGF MOTIF PROTEIN, EGFL6, MATERIALS AND METHODS

<130> 28110/37665

<140> US 09/981,649

<141> 2001-10-15

<150> US 09/687,860

<151> 2000-10-13

<150> US 09/620,312

<151> 2000-07-19

<150> US 09/363,316

<151> 1999-07-28

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gga tgt aag ttt ggt gag tgc gtg gga cca aac aaa tgc aga tgc ttt	96
Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe	
20 25 30	
cca gga tac acc ggg aaa acc tgc agt caa gat gtg aat gag tgt gga	144
Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly	
35 40 45	
atg aaa ccc cgg cca tgc caa cac aga tgt gtg aat aca cac gga agc	192
Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser	
50 55 60	

tac aag tgc ttt tgc ctc agt ggc cac atg ctc atg cca gat gct acg	240
Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr	
65 70 75 80	

tgt gtg aac tcn agg aca tgt gcc atg ata aac tgt cag tat agc tgt	288
Cys Val Asn Xaa Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys	
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gaa gac aca gaa	300
Glu Asp Thr Glu	
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1 5 10 15	

gga tgt aag ttt ggt gag tgc gtg gga cca aac aaa tgc aga tgc ttt	96
Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe	
20 25 30	

cca gga tac acc ggg aaa acc tgc agt caa gat gtg aat gag tgt gga	144
Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly	
35 40 45	

atg aaa ccc cgg cca tgc caa cac aga tgt gtg aat aca cac gga agc	192
Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser	
50 55 60	

tac aag tgc ttt tgc ctc agt ggc cac atg ctc atg cca gat gct acg	240
Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr	
65 70 75 80	

tgt	gtg	aac	tcn	agg	aca	tgt	gcc	atg	ata	aac	tgt	cag	tat	agc	tgt	288
Cys	Val	Asn	Xaa	Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	
				85					90					95		
gaa	gac	aca	gaa	gaa	ggg	cca	cag	tgc	ctg	tgt	cca	tcc	tca	gga	ctc	336
Glu	Asp	Thr	Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	
			100					105					110			
cgc	ctg	gcc	cca	aat	gga	aga	gac	tgt	cta	gat	att	gat	gaa	tgt	gcc	384
Arg	Leu	Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	
		115					120					125				
tct	ggg	aaa	gtc	atc	tgt	ccc	tac	aat	cga	aga	tgt	gtg	aac	aca	ttt	432
Ser	Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	
	130					135					140					
gga	agc	tac	tac	tgc	aaa	tgt	cac	att	ggg	ttc	gaa	ctg	caa	tat	atc	480
Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	Ile	
145					150				155						160	
agt	gga	cga	tat	gac	tgt	ata	gat	ata	aat	gaa	tgt	act	atg	gat	agc	528
Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met	Asp	Ser	
				165					170					175		
cat	acg	tgc	agc	cac	cat	gcc	aat	tgc	ttc	aat	acc	caa	ggg	tcc	ttc	576
His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln	Gly	Ser	Phe	
			180					185					190			
aag	tgt	aaa	tgc	aag	cag	gga	tat	aaa	ggc	aat	gga	ctt	cgg	tgt	tct	624
Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	Leu	Arg	Cys	Ser	
		195					200					205				
gct	atc	cct	gaa	aat	tct	gtg	aag	gaa	gtc	ctc	aga	gca	cct	ggg	acc	672
Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu	Arg	Ala	Pro	Gly	Thr	
	210					215					220					
atc	aaa	gac	aga	atc	aag	aag	ttg	ctt	gct	cac	aaa	aac	agc	atg	aaa	720
Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala	His	Lys	Asn	Ser	Met	Lys	
225					230				235						240	
aag	aag	gca	aaa	att	aaa	aat	gtt	acc	cca	gaa	ccc	acc	agg	act	cct	768
Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	Pro	Glu	Pro	Thr	Arg	Thr	Pro	
			245					250						255		
acc	cct	aag	gtg	aac	ttg	cag	ccc	ttc	aac	tat	gaa	gag	ata	gtt	tcc	816
Thr	Pro	Lys	Val	Asn	Leu	Gln	Pro	Phe	Asn	Tyr	Glu	Glu	Ile	Val	Ser	
			260					265					270			
aga	ggc	ggg	aac	tct	cat	gga	ggg	aaa	aaa	ggg	aat	gaa	gag	aaa	atg	864
Arg	Gly	Gly	Asn	Ser	His	Gly	Gly	Lys	Lys	Gly	Asn	Glu	Glu	Lys	Met	
		275					280					285				
aaa	gag	ggg	ctt	gag	gat	gag	aaa	aga	gaa	gag	aaa	gcc	ctg	aag	aat	912
Lys	Glu	Gly	Leu	Glu	Asp	Glu	Lys	Arg	Glu	Glu	Lys	Ala	Leu	Lys	Asn	
	290					295					300					
gac	ata	gag	gag	cga	agc	ctg	cga	gga	gat	gtg	ttt	ttc	cct	aag	gtg	960
Asp	Ile	Glu	Glu	Arg	Ser	Leu	Arg	Gly	Asp	Val	Phe	Phe	Pro	Lys	Val	
305					310					315					320	

aat gaa gca ggt gaa ttc ggc ctg att ctg gtc caa agg aaa gcg cta 1008  
Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg Lys Ala Leu  
325 330 335

act tcc aaa ctg gaa cat aaa gat tta aat atc tcg gtt gac tgc agc 1056  
Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser Val Asp Cys Ser  
340 345 350

ttc aat cat ggg atc tgt gac tgg aaa cag gat aga gaa gat gat ttt 1104  
Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe  
355 360 365

gac tgg aat cct gct gat cga gat aat gct att ggc ttc tat atg gca 1152  
Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala  
370 375 380

gtt ccg gcc ttg gca ggt cac atg aaa gac att ggc cga ttg aaa ctt 1200  
Val Pro Ala Leu Ala Gly His Met Lys Asp Ile Gly Arg Leu Lys Leu  
385 390 395 400

ctc cta cct gac ctg caa ccc caa agc aac ttc tgt ttg ctc ttt gat 1248  
Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp  
405 410 415

tac cgg ctg gcc gga gac aaa gtc ggg aaa ctt cga gtg ttt gtg aaa 1296  
Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg Val Phe Val Lys  
420 425 430

aac agt aac aat gcc ctg gca tgg gag aag acc acg agt gag gat gaa 1344  
Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr Ser Glu Asp Glu  
435 440 445

aag tgg aag aca ggg aaa att cag ttg tat caa gga act gat gct acc 1392  
Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly Thr Asp Ala Thr  
450 455 460

aaa agc atc att ttt gaa gca gaa cgt ggc aag ggc aaa acc ggc gaa 1440  
Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu  
465 470 475 480

atc gca gtg gat ggc gtc ttg ctt gtt tca ggc tta tgt cca gat agc 1488  
Ile Ala Val Asp Gly Val Leu Leu Val Ser Gly Leu Cys Pro Asp Ser  
485 490 495

ctt tta tct gtg gan nnc tgaatggtac tatctttata tttgactttg 1536  
Leu Leu Ser Val Xaa Xaa  
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Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly  
35 40 45

Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser  
 50 55 60  
 Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr  
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 85 90 95  
 Glu Asp Thr Glu  
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 35 40 45  
 Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser  
 50 55 60  
 Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr  
 65 70 75 80  
 Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys  
 85 90 95  
 Glu Asp Thr Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu  
 100 105 110  
 Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala  
 115 120 125  
 Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe  
 130 135 140  
 Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu Gln Tyr Ile  
 145 150 155 160  
 Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr Met Asp Ser  
 165 170 175  
 His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe  
 180 185 190  
 Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser  
 195 200 205  
 Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala Pro Gly Thr  
 210 215 220  
 Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn Ser Met Lys  
 225 230 235 240  
 Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr Arg Thr Pro  
 245 250 255  
 Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser  
 260 265 270  
 Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu Glu Lys Met  
 275 280 285  
 Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn  
 290 295 300  
 Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe Phe Pro Lys Val  
 305 310 315 320  
 Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg Lys Ala Leu  
 325 330 335

Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser Val Asp Cys Ser  
 340 345 350  
 Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe  
 355 360 365  
 Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala  
 370 375 380  
 Val Pro Ala Leu Ala Gly His Met Lys Asp Ile Gly Arg Leu Lys Leu  
 385 390 395 400  
 Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp  
 405 410 415  
 Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg Val Phe Val Lys  
 420 425 430  
 Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr Ser Glu Asp Glu  
 435 440 445  
 Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly Thr Asp Ala Thr  
 450 455 460  
 Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu  
 465 470 475 480  
 Ile Ala Val Asp Gly Val Leu Leu Val Ser Gly Leu Cys Pro Asp Ser  
 485 490 495  
 Leu Leu Ser Val Asp Asp Xaa Met Val Leu Ser Leu Tyr Leu Thr Leu  
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 Tyr Val Ser Ser Leu Val Phe Leu Ile Leu His His Arg Thr Ser Gly  
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Ile Leu Lys Leu Leu Ala Glu Lys Leu  
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 ggaggcggcg gcttagctgc tacgggggtcc ggccggcgcc ctcccagagg gggctcagga 180  
 ggaggaagga ggacccgtgc gaga atg cct ctg ccc tgg agc ctt gcg ctc 231  
 Met Pro Leu Pro Trp Ser Leu Ala Leu  
 1 5  
 ccg ctg ctg ctc ccc tgg gtg gca ggt ggt ttc ggg aac gcg gcc agt 279  
 Pro Leu Leu Leu Pro Trp Val Ala Gly Gly Phe Gly Asn Ala Ala Ser  
 10 15 20 25  
 gca agg cat cac ggg ttg tta gca tcg gca cgt cag cct ggg gtc tgt 327  
 Ala Arg His His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly Val Cys  
 30 35 40  
 cac tat gga act aaa ctg gcc tgc tgc tac ggc tgg aga aga aac agc 375  
 His Tyr Gly Thr Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser  
 45 50 55

aag gga gtc tgt gaa gct aca tgc gaa cct gga tgt aag ttt ggt gag	423
Lys Gly Val Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu	
60 65 70	
tgc gtg gga cca aac aaa tgc aga tgc ttt cca gga tac acc ggg aaa	471
Cys Val Gly Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys	
75 80 85	
acc tgc agt caa gat gtg aat gag tgt gga atg aaa ccc cgg cca tgc	519
Thr Cys Ser Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg Pro Cys	
90 95 100 105	
caa cac aga tgt gtg aat aca cac gga agc tac aag tgc ttt tgc ctc	567
Gln His Arg Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe Cys Leu	
110 115 120	
agt ggc cac atg ctc atg cca gat gct acg tgt gtg aac tct agg aca	615
Ser Gly His Met Leu Met Pro Asp Ala Thr Cys Val Asn Ser Arg Thr	
125 130 135	
tgt gcc atg ata aac tgt cag tat agc tgt gaa gac aca gaa gaa ggg	663
Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr Glu Glu Gly	
140 145 150	
cca cag tgc ctg tgt cca tcc tca gga ctc cgc ctg gcc cca aat gga	711
Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu Arg Leu Ala Pro Asn Gly	
155 160 165	
aga gac tgt cta gat att gat gaa tgt gcc tct ggt aaa gtc atc tgt	759
Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala Ser Gly Lys Val Ile Cys	
170 175 180 185	
ccc tac aat cga aga tgt gtg aac aca ttt gga agc tac tac tgc aaa	807
Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys	
190 195 200	
tgt cac att ggt ttc gaa ctg caa tat atc agt gga cga tat gac tgt	855
Cys His Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Tyr Asp Cys	
205 210 215	
ata gat ata aat gaa tgt act atg gat agc cat acg tgc agc cac cat	903
Ile Asp Ile Asn Glu Cys Thr Met Asp Ser His Thr Cys Ser His His	
220 225 230	
gcc aat tgc ttc aat acc caa ggg tcc ttc aag tgt aaa tgc aag cag	951
Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe Lys Cys Lys Cys Lys Gln	
235 240 245	
gga tat aaa ggc aat gga ctt cgg tgt tct gct atc cct gaa aat tct	999
Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser Ala Ile Pro Glu Asn Ser	
250 255 260 265	
gtg aag gaa gtc ctc aga gca cct ggt acc atc aaa gac aga atc aag	1047
Val Lys Glu Val Leu Arg Ala Pro Gly Thr Ile Lys Asp Arg Ile Lys	
270 275 280	
aag ttg ctt gct cac aaa aac agc atg aaa aag aag gca aaa att aaa	1095
Lys Leu Leu Ala His Lys Asn Ser Met Lys Lys Lys Ala Lys Ile Lys	
285 290 295	

aat gtt acc cca gaa ccc acc agg act cct acc cct aag gtg aac ttg	1143
Asn Val Thr Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu	
300 305 310	
cag ccc ttc aac tat gaa gag ata gtt tcc aga ggc ggg aac tct cat	1191
Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His	
315 320 325	
gga ggt aaa aaa ggg aat gaa gag aaa atg aaa gag ggg ctt gag gat	1239
Gly Gly Lys Lys Gly Asn Glu Glu Lys Met Lys Lys Glu Gly Leu Glu Asp	
330 335 340 345	
gag aaa aga gaa gag aaa gcc ctg aag aat gac wta gag gag cga agc	1287
Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn Asp Xaa Glu Glu Arg Ser	
350 355 360	
ctg cga gga gat gtg ttt ttc cct aag gtg aat gaa gca ggt gaa ttc	1335
Leu Arg Gly Asp Val Phe Phe Pro Lys Val Asn Glu Ala Gly Glu Phe	
365 370 375	
ggc ctg att ctg gtc caa agg aaa gcg cta act tcc aaa ctg gaa cat	1383
Gly Leu Ile Leu Val Gln Arg Lys Ala Leu Thr Ser Lys Leu Glu His	
380 385 390	
aaa gat tta aat atc tcg gtt gac tgc agc ttc aat cat ggg atc tgt	1431
Lys Asp Leu Asn Ile Ser Val Asp Cys Ser Phe Asn His Gly Ile Cys	
395 400 405	
gac tgg aaa cag gat aga gaa gat gat ttt gac tgg aat cct gct gat	1479
Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp	
410 415 420 425	
cga gat aat gct att ggc ttc tat atg gca gtt ccg gcc ttg gca ggt	1527
Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala Val Pro Ala Leu Ala Gly	
430 435 440	
cac aag aaa gac att ggc cga ttg aaa ctt ctc cta cct gac ctg caa	1575
His Lys Lys Asp Ile Gly Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln	
445 450 455	
ccc caa agc aac ttc tgt ttg ctc ttt gat tac cgg ctg gcc gga gac	1623
Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp	
460 465 470	
aaa gtc ggg aaa ctt cga gtg ttt gtg aaa aac agt aac aat gcc ctg	1671
Lys Val Gly Lys Leu Arg Val Phe Val Lys Asn Ser Asn Asn Ala Leu	
475 480 485	
gca tgg gag aag acc acg agt gag gat gaa aag tgg aag aca ggg aaa	1719
Ala Trp Glu Lys Thr Thr Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys	
490 495 500 505	
att cag ttg tat caa gga act gat gct acc aaa agc atc att ttt gaa	1767
Ile Gln Leu Tyr Gln Gly Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu	
510 515 520	
gca gaa cgt ggc aag ggc aaa acc ggc gaa atc gca gtg gat ggc gtc	1815
Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu Ile Ala Val Asp Gly Val	
525 530 535	
ttg ctt gtt tca ggc tta tgt cca gat agc ctt tta tct gtg gat gac	1863
Leu Leu Val Ser Gly Leu Cys Pro Asp Ser Leu Leu Ser Val Asp Asp	
540 545 550	



tga atgttactat ctttatatatt gactttgtat gtcagttccc tggttttttt 1916  
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ccaacagaaa ttattattgt aagatgcctt tmttgtataa gatatgccaa tatttgcttt 2036  
aaatatcata tcaactgtatc ttctcagtc tttctgaatc tttccacatt atattataaa 2096  
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ctgtttgact cttatgatag tttttggaaa ctatgacatc aaagatagac ttttgcctaa 2276  
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Ala Ser Ala Arg Gln Pro Gly Val Cys His Tyr Gly Thr Lys Leu Ala  
35 40 45  
  
Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr  
50 55 60  
Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys  
65 70 75 80  
Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn  
85 90 95  
Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr  
100 105 110  
His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro  
115 120 125  
Asp Ala Thr Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln  
130 135 140  
Tyr Ser Cys Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser  
145 150 155 160  
Ser Gly Leu Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp  
165 170 175  
Glu Cys Ala Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val  
180 185 190  
Asn Thr Phe Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu  
195 200 205  
Gln Tyr Ile Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr  
210 215 220  
Met Asp Ser His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln  
225 230 235 240  
Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu  
245 250 255  
Arg Cys Ser Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala  
260 265 270  
Pro Gly Thr Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn  
275 280 285  
Ser Met Lys Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr  
290 295 300

Arg	Thr	Pro	Thr	Pro	Lys	Val	Asn	Leu	Gln	Pro	Phe	Asn	Tyr	Glu	Glu
305					310					315					320
Ile	Val	Ser	Arg	Gly	Gly	Asn	Ser	His	Gly	Gly	Lys	Lys	Gly	Asn	Glu
				325					330					335	
Glu	Lys	Met	Lys	Glu	Gly	Leu	Glu	Asp	Glu	Lys	Arg	Glu	Glu	Lys	Ala
			340					345					350		
Leu	Lys	Asn	Asp	Xaa	Glu	Glu	Arg	Ser	Leu	Arg	Gly	Asp	Val	Phe	Phe
		355					360					365			
Pro	Lys	Val	Asn	Glu	Ala	Gly	Glu	Phe	Gly	Leu	Ile	Leu	Val	Gln	Arg
	370					375					380				
Lys	Ala	Leu	Thr	Ser	Lys	Leu	Glu	His	Lys	Asp	Leu	Asn	Ile	Ser	Val
385					390					395					400
Asp	Cys	Ser	Phe	Asn	His	Gly	Ile	Cys	Asp	Trp	Lys	Gln	Asp	Arg	Glu
				405					410					415	
Asp	Asp	Phe	Asp	Trp	Asn	Pro	Ala	Asp	Arg	Asp	Asn	Ala	Ile	Gly	Phe
			420					425					430		
Tyr	Met	Ala	Val	Pro	Ala	Leu	Ala	Gly	His	Lys	Lys	Asp	Ile	Gly	Arg
	435						440						445		
Leu	Lys	Leu	Leu	Leu	Pro	Asp	Leu	Gln	Pro	Gln	Ser	Asn	Phe	Cys	Leu
	450					455					460				
Leu	Phe	Asp	Tyr	Arg	Leu	Ala	Gly	Asp	Lys	Val	Gly	Lys	Leu	Arg	Val
465					470					475					480
Phe	Val	Lys	Asn	Ser	Asn	Asn	Ala	Leu	Ala	Trp	Glu	Lys	Thr	Thr	Ser
				485					490					495	
Glu	Asp	Glu	Lys	Trp	Lys	Thr	Gly	Lys	Ile	Gln	Leu	Tyr	Gln	Gly	Thr
			500					505					510		
Asp	Ala	Thr	Lys	Ser	Ile	Ile	Phe	Glu	Ala	Glu	Arg	Gly	Lys	Gly	Lys
	515						520					525			
Thr	Gly	Glu	Ile	Ala	Val	Asp	Gly	Val	Leu	Leu	Val	Ser	Gly	Leu	Cys
	530					535					540				

Pro Asp Ser Leu Leu Ser Val Asp Asp  
545 550

<210> 7  
 <211> 42  
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 Ile Asp Glu Cys Xaa Ser Asn Pro Cys Gln Asn Gly Gly Thr Cys Xaa  
 1 5 10 15  
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 20 25 30  
 Thr Gly Lys Xaa Xaa Xaa Cys Glu Xaa Asn  
 35 40

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 <211> 39  
 <212> PRT  
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Xaa Asn Glu Cys Thr Met Xaa Xaa Xaa Cys Gln His Xaa Xaa Xaa Cys
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 20          25          30
Gly Xaa Xaa Leu Xaa Cys Asp
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<210> 9  
 <211> 164  
 <212> PRT  
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<400> 9  
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 Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr  
 20 25 30  
 His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro  
 35 40 45  
 Asp Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys  
 50 55 60  
 Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu  
 65 70 75 80  
 Arg Leu Ala Pro Asn Ile Asp Glu Cys Ala Ser Gly Lys Val Ile Cys  
 85 90 95  
 Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys  
 100 105 110  
 Cys His Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Ile Asn Glu  
 115 120 125  
 Cys Thr Met Asp Ser His Thr Cys Ser His His Ala Asn Cys Phe Asn  
 130 135 140  
 Thr Gln Gly Ser Phe Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly  
 145 150 155 160  
 Leu Arg Cys Ser

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 1 5 10 15  
 Xaa Cys Xaa Asn Thr Val Gly Ser Tyr Xaa Cys Arg Cys Arg Pro Gly  
 20 25 30  
 Trp Xaa Pro Xaa Pro Gly Xaa Pro Asn Xaa Xaa Xaa Asp  
 35 40 45

<210> 11  
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<400> 11  
 Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His  
 1 5 10 15  
 Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn  
 20 25 30  
 Cys Val Val Gly Tyr Ile Xaa Xaa Xaa Gly Glu Arg Xaa Xaa Cys Gln  
 35 40 45  
 Tyr Arg Asp Leu Lys Trp Trp Glu Leu Arg  
 50 55

<210> 12  
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 <212> DNA  
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<220>  
 <223> Gene-specific PCR primer 10244-52

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 ctcatactca agccctctt t

21

<210> 13  
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 ccatgagagt tcccgcctct g

21

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<210> 14
<211> 21
<212> DNA
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<220>
<223> Vector primer T7

<400> 14
gtaatacgac tcactatagg g                                21

<210> 15
<211> 22
<212> DNA
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<220>
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<400> 15
atttaggtga cactatagaa gg                                22

<210> 16
<211> 21
<212> DNA
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<220>
<223> Gene-specific PCR primer 10244-A

<400> 16
cccaggctga cgtgccgatg c                                21

<210> 17
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Gene-specific PCR primer 10244-B

<400> 17
gcagcaggcc agttagttc c                                21

<210> 18
<211> 502
<212> PRT
<213> Homo sapiens

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 1          5          10          15

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Pro	Gly	Tyr	Thr	Gly	Lys	Thr	Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	35	40	45
Met	Lys	Pro	Arg	Pro	Cys	Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	50	55	60
Tyr	Lys	Cys	Phe	Cys	Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	65	70	75
Cys	Val	Asn	Ser	Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	85	90	95
Glu	Asp	Thr	Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	100	105	110
Arg	Leu	Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	115	120	125
Ser	Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	130	135	140
Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	Ile	145	150	155
Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met	Asp	Ser	165	170	175
His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln	Gly	Ser	Phe	180	185	190
Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	Leu	Arg	Cys	Ser	195	200	205
Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu	Arg	Ala	Pro	Gly	Thr	210	215	220
Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala	His	Lys	Asn	Ser	Met	Lys	225	230	235
Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	Pro	Glu	Pro	Thr	Arg	Thr	Pro	245	250	255
Thr	Pro	Lys	Val	Asn	Leu	Gln	Pro	Phe	Asn	Tyr	Glu	Glu	Ile	Val	Ser	260	265	270
Arg	Gly	Gly	Asn	Ser	His	Gly	Gly	Lys	Lys	Gly	Asn	Glu	Glu	Lys	Met	275	280	285
Lys	Glu	Gly	Leu	Glu	Asp	Glu	Lys	Arg	Glu	Glu	Lys	Ala	Leu	Lys	Asn	290	295	300
Asp	Ile	Glu	Glu	Arg	Ser	Leu	Arg	Gly	Asp	Val	Phe	Phe	Pro	Lys	Val	305	310	315
Asn	Glu	Ala	Gly	Glu	Phe	Gly	Leu	Ile	Leu	Val	Gln	Arg	Lys	Ala	Leu	325	330	335
Thr	Ser	Lys	Leu	Glu	His	Lys	Asp	Leu	Asn	Ile	Ser	Val	Asp	Cys	Ser	340	345	350
Phe	Asn	His	Gly	Ile	Cys	Asp	Trp	Lys	Gln	Asp	Arg	Glu	Asp	Asp	Phe	355	360	365
Asp	Trp	Asn	Pro	Ala	Asp	Arg	Asp	Asn	Ala	Ile	Gly	Phe	Tyr	Met	Ala	370	375	380
Val	Pro	Ala	Leu	Ala	Gly	His	Met	Lys	Asp	Ile	Gly	Arg	Leu	Lys	Leu	385	390	395
Leu	Leu	Pro	Asp	Leu	Gln	Pro	Gln	Ser	Asn	Phe	Cys	Leu	Leu	Phe	Asp	405	410	415
Tyr	Arg	Leu	Ala	Gly	Asp	Lys	Val	Gly	Lys	Leu	Arg	Val	Phe	Val	Lys	420	425	430
Asn	Ser	Asn	Asn	Ala	Leu	Ala	Trp	Glu	Lys	Thr	Thr	Ser	Glu	Asp	Glu	435	440	445
Lys	Trp	Lys	Thr	Gly	Lys	Ile	Gln	Leu	Tyr	Gln	Gly	Thr	Asp	Ala	Thr	450	455	460
Lys	Ser	Ile	Ile	Phe	Glu	Ala	Glu	Arg	Gly	Lys	Gly	Lys	Thr	Gly	Glu	465	470	475
Ile	Ala	Val	Asp	Gly	Val	Leu	Leu	Val	Ser	Gly	Leu	Cys	Pro	Asp	Ser	485	490	495
Leu	Leu	Ser	Val	Xaa	Xaa											500		

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<210> 21
<211> 20
<212> DNA
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<220>
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ccagaaccca ccaggactcc                               20

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ggaggcggcg gcttagctgc tacgggggtcc ggccggcgcc ctcccagagg gggctcagga 180
ggaggaagga ggacccgtgc gaga atg cct ctg ccc tgg agc ctt gcg ctc      231
Met Pro Leu Pro Trp Ser Leu Ala Leu
1                               5

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ccg ctg ctg ctc tcc tgg gtg gca ggt ggt ttc ggg aac gcg gcc agt	279
Pro Leu Leu Leu Ser Trp Val Ala Gly Gly Phe Gly Asn Ala Ala Ser	
10 15 20 25	
gca agg cat cac ggg ttg tta gca tcg gca cgt cag cct ggg gtc tgt	327
Ala Arg His His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly Val Cys	
30 35 40	
cac tat gga act aaa ctg gcc tgc tgc tac ggc tgg aga aga aac agc	375
His Tyr Gly Thr Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser	
45 50 55	
aag gga gtc tgt gaa gct aca tgc gaa cct gga tgt aag ttt ggt gag	423
Lys Gly Val Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu	
60 65 70	
tgc gtg gga cca aac aaa tgc aga tgc ttt cca gga tac acc ggg aaa	471
Cys Val Gly Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys	
75 80 85	
acc tgc agt caa gat gtg aat gag tgt gga atg aaa ccc cgg cca tgc	519
Thr Cys Ser Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg Pro Cys	
90 95 100 105	
caa cac aga tgt gtg aat aca cac gga agc tac aag tgc ttt tgc ctc	567
Gln His Arg Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe Cys Leu	
110 115 120	
agt ggc cac atg ctc atg cca gat gct acg tgt gtg aac tct agg aca	615
Ser Gly His Met Leu Met Pro Asp Ala Thr Cys Val Asn Ser Arg Thr	
125 130 135	
tgt gcc atg ata aac tgt cag tat agc tgt gaa gac aca gaa gaa ggg	663
Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr Glu Glu Gly	
140 145 150	
cca cag tgc ctg tgt cca tcc tca gga ctc cgc ctg gcc cca aat gga	711
Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu Arg Leu Ala Pro Asn Gly	
155 160 165	
aga gac tgt cta gat att gat gaa tgt gcc tct ggt aaa gtc atc tgt	759
Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala Ser Gly Lys Val Ile Cys	
170 175 180 185	
ccc tac aat cga aga tgt gtg aac aca ttt gga agc tac tac tgc aaa	807
Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys	
190 195 200	
tgt cac att ggt ttc gaa ctg caa tat atc agt gga cga tat gac tgt	855
Cys His Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Tyr Asp Cys	
205 210 215	
ata gat ata aat gaa tgt act atg gat agc cat acg tgc agc cac cat	903
Ile Asp Ile Asn Glu Cys Thr Met Asp Ser His Thr Cys Ser His His	
220 225 230	
gcc aat tgc ttc aat acc caa ggg tcc ttc aag tgt aaa tgc aag cag	951
Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe Lys Cys Lys Cys Lys Gln	
235 240 245	

gga tat aaa ggc aat gga ctt cgg tgt tct gct atc cct gaa aat tct	999
Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser Ala Ile Pro Glu Asn Ser	
250 255 260 265	
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Val Lys Glu Val Leu Arg Ala Pro Gly Thr Ile Lys Asp Arg Ile Lys	
270 275 280	
aag ttg ctt gct cac aaa aac agc atg aaa aag aag gca aaa att aaa	1095
Lys Leu Leu Ala His Lys Asn Ser Met Lys Lys Lys Ala Lys Ile Lys	
285 290 295	
aat gtt acc cca gaa ccc acc agg act cct acc cct aag gtg aac ttg	1143
Asn Val Thr Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu	
300 305 310	
cag ccc ttc aac tat gaa gag ata gtt tcc aga ggc ggg aac tct cat	1191
Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His	
315 320 325	
gga ggt aaa aaa ggg aat gaa gag aaa atg aaa gag ggg ctt gag gat	1239
Gly Gly Lys Lys Gly Asn Glu Glu Lys Met Lys Glu Gly Leu Glu Asp	
330 335 340 345	
gag aaa aga gaa gag aaa gcc ctg aag aat gac ata gag gag cga agc	1287
Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn Asp Ile Glu Glu Arg Ser	
350 355 360	
ctg cga gga gat gtg ttt ttc cct aag gtg aat gaa gca ggt gaa ttc	1335
Leu Arg Gly Asp Val Phe Phe Pro Lys Val Asn Glu Ala Gly Glu Phe	
365 370 375	
ggc ctg att ctg gtc caa agg aaa gcg cta act tcc aaa ctg gaa cat	1383
Gly Leu Ile Leu Val Gln Arg Lys Ala Leu Thr Ser Lys Leu Glu His	
380 385 390	
aaa gat tta aat atc tcg gtt gac tgc agc ttc aat cat ggg atc tgt	1431
Lys Asp Leu Asn Ile Ser Val Asp Cys Ser Phe Asn His Gly Ile Cys	
395 400 405	
gac tgg aaa cag gat aga gaa gat gat ttt gac tgg aat cct gct gat	1479
Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp	
410 415 420 425	
cga gat aat gct att ggc ttc tat atg gca gtt ccg gcc ttg gca ggt	1527
Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala Val Pro Ala Leu Ala Gly	
430 435 440	
cac aag aaa gac att ggc cga ttg aaa ctt ctc cta cct gac ctg caa	1575
His Lys Lys Asp Ile Gly Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln	
445 450 455	
ccc caa agc aac ttc tgt ttg ctc ttt gat tac cgg ctg gcc gga gac	1623
Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp	
460 465 470	
aaa gtc ggg aaa ctt cga gtg ttt gtg aaa aac agt aac aat gcc ctg	1671
Lys Val Gly Lys Leu Arg Val Phe Val Lys Asn Ser Asn Asn Ala Leu	
475 480 485	
gca tgg gag aag acc acg agt gag gat gaa aag tgg aag aca ggg aaa	1719
Ala Trp Glu Lys Thr Thr Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys	
490 495 500 505	

att cag ttg tat caa gga act gat gct acc aaa agc atc att ttt gaa 1767  
Ile Gln Leu Tyr Gln Gly Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu  
510 515 520

gca gaa cgt ggc aag ggc aaa acc ggc gaa atc gca gtg gat ggc gtc 1815  
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525 530 535

ttg ctt gtt tca ggc tta tgt cca gat agc ctt tta tct gtg gat gac 1863  
Leu Leu Val Ser Gly Leu Cys Pro Asp Ser Leu Leu Ser Val Asp Asp  
540 545 550

tgaatgttac tatctttata tttgactttg tatgtcagtt ccctgggtttt tttgatattg 1923

satcatagga cctctggcat tttaaaatta ctaagctgaa aaattgtaat gtaccaacag 1983

aaattattat tgtaagatgc ctttmttgta taagatatgc caatatttgc tttaaatatc 2043

atatcactgt atcttctcag tcatttctga atctttccac attatattat aaaatatgga 2103

aatgtcaggt ttatctcccc tcttcagtat atctgatttg tataagtaag ttgatgagct 2163

tctctctgca acatttctag aaaatagaha aaaaagcaca gagaaatgtt taactgtttg 2223

actcttatga tagttttttg aaactatgac atcaaagata gacttttgcc taagtggctt 2283

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Ala Ser Ala Arg Gln Pro Gly Val Cys His Tyr Gly Thr Lys Leu Ala  
35 40 45  
Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr  
50 55 60  
Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys  
65 70 75 80  
Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn  
85 90 95  
Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr  
100 105 110

His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro  
115 120 125

Asp Ala Thr Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln  
130 135 140

Tyr Ser Cys Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser  
145 150 155 160

Ser Gly Leu Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp  
165 170 175

Glu Cys Ala Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val  
180 185 190

Asn Thr Phe Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu  
195 200 205

Gln Tyr Ile Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr  
210 215 220

Met Asp Ser His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln  
225 230 235 240

Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu  
245 250 255

Arg Cys Ser Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala  
260 265 270

Pro Gly Thr Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn  
275 280 285

Ser Met Lys Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr  
290 295 300

Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu  
305 310 315 320

Ile Val Ser Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu  
325 330 335

Glu Lys Met Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala  
340 345 350

Leu Lys Asn Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe Phe  
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Pro Lys Val Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg  
370 375 380

Lys Ala Leu Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser Val  
385 390 395 400

Asp Cys Ser Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg Glu  
405 410 415

Asp Asp Phe Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly Phe  
420 425 430

Tyr Met Ala Val Pro Ala Leu Ala Gly His Lys Lys Asp Ile Gly Arg  
435 440 445

Leu Lys Leu Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys Leu  
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Leu Phe Asp Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg Val  
 465 470 475 480

Phe Val Lys Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr Ser  
 485 490 495

Glu Asp Glu Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly Thr  
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Asp Ala Thr Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly Lys  
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ctgctacggg gtccgggccc gcgccctccc gaggggggct caggaggagg aaggaggacc      180
cgtgcgaga      atg cct ctg ccc tgg agc ctt gcg ctc ccg ctg ctg ctc      228
                Met Pro Leu Pro Trp Ser Leu Ala Leu Pro Leu Leu Leu
                1          5          10

tcc tgg gtg gca ggt ggt ttc ggg aac gcg gcc agt gca agg ggt tct      276
Ser Trp Val Ala Gly Gly Phe Gly Asn Ala Ala Ser Ala Arg Gly Ser
14          19          24          29

cat cat cat cat cat cac ggg ttg tta gca tgc gca cgt cag cct ggg      324
His His His His His His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly
30          35          40          45

gtc tgt cac tat gga act aaa ctg gcc tgc tgc tac ggc tgg aga aga      372
Val Cys His Tyr Gly Thr Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg
46          51          56          61

aac agc aag gga gtc tgt gaa gct aca tgc gaa cct gga tgt aag ttt      420
Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe
62          67          72          77

ggg gag tgc gtg gga cca aac aaa tgc aga tgc ttt cca gga tac acc      468
Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr
78          83          88          93

ggg aaa acc tgc agt caa gat gtg aat gag tgt gga atg aaa ccc cgg      516
Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg
94          99          104          109

cca tgc caa cac aga tgt gtg aat aca cac gga agc tac aag tgc ttt      564
Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe
110          115          120          125

tgc ctc agt ggc cac atg ctc atg cca gat gct acg tgt gtg aac tct      612
Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr Cys Val Asn Ser
126          131          136          141

agg aca tgt gcc atg ata aac tgt cag tac agc tgt gaa gac aca gaa      660
Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr Glu
142          147          152          157

gaa ggg cca cag tgc ctg tgt cca tcc tca gga ctc cgc ctg gcc cca      708
Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu Arg Leu Ala Pro
158          163          168          173

aat gga aga gac tgt cta gat att gat gaa tgt gcc tct ggt aaa gtc      756
Asn Gly Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala Ser Gly Lys Val
174          179          184          189

atc tgt ccc tac aat cga aga tgt gtg aac aca ttt gga agc tac tac      804
Ile Cys Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr
190          195          200          205

tgc aaa tgt cac att ggt ttc gaa ctg caa tat atc agt gga cga tat      852
Cys Lys Cys His Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Tyr
206          211          216          221

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His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln	Gly	Ser	Phe	Lys	Cys	Lys	Cys	
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Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	
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Glu	Asp	Glu	Lys	Arg	Glu	Glu	Lys	Ala	Leu	Lys	Asn	Asp	Ile	Glu	Glu	
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Arg	Ser	Leu	Arg	Gly	Asp	Val	Phe	Phe	Pro	Lys	Val	Asn	Glu	Ala	Gly	
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gaa	ttc	ggc	ctg	att	ctg	gtc	caa	agg	aaa	gcg	cta	act	tcc	aaa	ctg	1380
Glu	Phe	Gly	Leu	Ile	Leu	Val	Gln	Arg	Lys	Ala	Leu	Thr	Ser	Lys	Leu	
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Ala	Gly	His	Lys	Lys	Asp	Ile	Gly	Arg	Leu	Lys	Leu	Leu	Leu	Pro	Asp	
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ctg	caa	ccc	caa	agc	aac	ttc	tgt	ttg	ctc	ttt	gat	tac	cgg	ctg	gcc	1620
Leu	Gln	Pro	Gln	Ser	Asn	Phe	Cys	Leu	Leu	Phe	Asp	Tyr	Arg	Leu	Ala	
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gcc ctg gca tgg gag aag acc acg agt gag gat gaa aag tgg aag aca 1716  
Ala Leu Ala Trp Glu Lys Thr Thr Ser Glu Asp Glu Lys Trp Lys Thr  
494 499 504 509

ggg aaa att cag ttg tat caa gga act gat gct acc aaa agc atc att 1764  
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510 515 520 525

ttt gaa gca gaa cgt ggc aag ggc aaa acc ggc gaa atc gca gtg gat 1812  
Phe Glu Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu Ile Ala Val Asp  
526 531 536 541

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Gly Val Leu Leu Val Ser Gly Leu Cys Pro Asp Ser Leu Leu Ser Val  
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gat gac tga atgttac tatctttata ttgactttg tatgtcagtt ccttggtttt 1916  
Asp Asp \*  
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taaatatcat atcactgtat cttctcagtc atttctgaat cttccacat tatattataa 2096

aatatggaaa tgtcagttta tctccctcc tcagtatatc tgatttgtat aagtaagttg 2156

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His His His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly Val Cys His  
35 40 45

Tyr Gly Thr Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys  
50 55 60

Gly Val Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys  
65 70 75 80

Val	Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	85	90	95
Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	Gln	100	105	110
His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	Leu	Ser	115	120	125
Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser	Arg	Thr	Cys	130	135	140
Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr	Glu	Glu	Gly	Pro	145	150	155
Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu	Ala	Pro	Asn	Gly	Arg	165	170	175
Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser	Gly	Lys	Val	Ile	Cys	Pro	180	185	190
Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	195	200	205
His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	210	215	220
Asp	Ile	Asn	Glu	Cys	Thr	Met	Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	225	230	235
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Tyr	Lys	Gly	Asn	Gly	Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	260	265	270
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Pro	Phe	Asn	Tyr	Glu	Glu	Ile	Val	Ser	Arg	Gly	Gly	Asn	Ser	His	Gly	325	330	335
Gly	Lys	Lys	Gly	Asn	Glu	Glu	Lys	Met	Lys	Glu	Gly	Leu	Glu	Asp	Glu	340	345	350
Lys	Arg	Glu	Glu	Lys	Ala	Leu	Lys	Asn	Asp	Ile	Glu	Glu	Arg	Ser	Leu	355	360	365
Arg	Gly	Asp	Val	Phe	Phe	Pro	Lys	Val	Asn	Glu	Ala	Gly	Glu	Phe	Gly	370	375	380
Leu	Ile	Leu	Val	Gln	Arg	Lys	Ala	Leu	Thr	Ser	Lys	Leu	Glu	His	Lys	385	390	395
Asp	Leu	Asn	Ile	Ser	Val	Asp	Cys	Ser	Phe	Asn	His	Gly	Ile	Cys	Asp	405	410	415

Trp Lys Gln Asp Arg Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp Arg  
420 425 430

Asp Asn Ala Ile Gly Phe Tyr Met Ala Val Pro Ala Leu Ala Gly His  
435 440 445

Lys Lys Asp Ile Gly Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln Pro  
450 455 460

Gln Ser Asn Phe Cys Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp Lys  
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Val Gly Lys Leu Arg Val Phe Val Lys Asn Ser Asn Asn Ala Leu Ala  
485 490 495

Trp Glu Lys Thr Thr Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys Ile  
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Gln Leu Tyr Gln Gly Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu Ala  
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Met Pro Leu Pro Trp Ser Leu Ala Leu Pro Leu Leu Leu  
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His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly Val Cys His Tyr Gly  
30 35 40 45

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Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	Gly	
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Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	Cys	Ser	
78					83					88					93	
caa	gat	gtg	aat	gag	tgt	gga	atg	aaa	ccc	cgg	cca	tgc	caa	cac	aga	516
Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	Gln	His	Arg	
94					99					104					109	
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Cys	Val	Asn	Thr	His		Ser	Tyr	Lys	Cys	Phe	Cys	Leu	Ser	Gly	His	
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Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser	Arg	Thr	Cys	Ala	Met	
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Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu	Ala	Pro	Asn	Gly	Arg	Asp	Cys	
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Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser	Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	
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Gly	Asn	Gly	Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	
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Val	Leu	Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	
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gct	cac	aaa	aac	agt	atg	aaa	aag	aag	gca	aaa	att	aaa	aat	gtt	acc	1092
Ala	His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	
286					291					296					301	

cca gaa ccc acc agg act cct acc cct aag gtg aac ttg cag ccc ttc	1140
Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro Phe	
302 307 312 317	
aac tat gaa gag ata gtt tcc aga ggc ggg aac tct cat gga ggt aaa	1188
Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly Gly Lys	
318 323 328 333	
aaa ggg aat gaa gag aaa atg aaa gag ggg ctt gag gat gag aaa aga	1236
Lys Gly Asn Glu Glu Lys Met Lys Glu Gly Leu Glu Asp Glu Lys Arg	
334 339 344 349	
gaa gag aaa gcc ctg aag aat gac ata gag gag cga agc ctg cga gga	1284
Glu Glu Lys Ala Leu Lys Asn Asp Ile Glu Glu Arg Ser Leu Arg Gly	
350 355 360 365	
gat gtg ttt ttc cct aag gtg aat gaa gca ggt gaa ttc ggc ctg att	1332
Asp Val Phe Phe Pro Lys Val Asn Glu Ala Gly Glu Phe Gly Leu Ile	
366 371 376 381	
ctg gtc caa agg aaa gcg cta act tcc aaa ctg gaa cat aaa gat tta	1380
Leu Val Gln Arg Lys Ala Leu Thr Ser Lys Leu Glu His Lys Asp Leu	
382 387 392 397	
aat atc tcg gtt gac tgc agc ttc aat cat ggg atc tgt gac tgg aaa	1428
Asn Ile Ser Val Asp Cys Ser Phe Asn His Gly Ile Cys Asp Trp Lys	
398 403 408 413	
cag gat aga gaa gat gat ttt gac tgg aat cct gct gat cga gat aat	1476
Gln Asp Arg Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp Arg Asp Asn	
414 419 424 429	
gct att ggc ttc tat atg gca gtt ccg gcc ttg gca ggt cac aag aaa	1524
Ala Ile Gly Phe Tyr Met Ala Val Pro Ala Leu Ala Gly His Lys Lys	
430 435 440 445	
gac att ggc cga ttg aaa ctt ctc cta cct gac ctg caa ccc caa agc	1572
Asp Ile Gly Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln Pro Gln Ser	
446 451 456 461	
aac ttc tgt ttg ctc ttt gat tac cgg ctg gcc gga gac aaa gtc ggg	1620
Asn Phe Cys Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp Lys Val Gly	
462 467 472 477	
aaa ctt cga gtg ttt gtg aaa aac agt aac aat gcc ctg gca tgg gag	1668
Lys Leu Arg Val Phe Val Lys Asn Ser Asn Asn Ala Leu Ala Trp Glu	
478 483 488 493	
aag acc acg agt gag gat gaa aag tgg aag aca ggg aaa att cag ttg	1716
Lys Thr Thr Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys Ile Gln Leu	
494 499 504 509	
tat caa gga act gat gct acc aaa agc atc att ttt gaa gca gaa cgt	1764
Tyr Gln Gly Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu Ala Glu Arg	
510 515 520 525	
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Gly Lys Gly Lys Thr Gly Glu Ile Ala Val Asp Gly Val Leu Leu Val	
526 531 536 541	
tca ggc tta tgt cca gat agc ctt tta tct gtg gat gac tga atgttac	1861
Ser Gly Leu Cys Pro Asp Ser Leu Leu Ser Val Asp Asp *	
542 547 552	

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cctctggcat tttagaatta ctagctgaaa aattgtaatg taccaacaga aatattattg 1981  
taagatgcct ttcttgtata agatatgcca atatttgctt taaatatcat atcactgtat 2041  
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tctccctcc tcagtataat tgatttgat aagtaagttg atgagcttct ctctacaaca 2161  
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aaaa 2345

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<212> PRT  
<213> Homo sapiens

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Leu Ala Ser Ala Arg Gln Pro Gly Val Cys His Tyr Gly Thr Lys Leu  
35 40 45  
Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala  
50 55 60  
Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys  
65 70 75 80  
Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val  
85 90 95  
Asn Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn  
100 105 110  
Thr His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met  
115 120 125  
Pro Asp Ala Thr Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys  
130 135 140  
Gln Tyr Ser Cys Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro  
145 150 155 160  
Ser Ser Gly Leu Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile  
165 170 175  
Asp Glu Cys Ala Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys  
180 185 190

Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu  
195 200 205

Leu Gln Tyr Ile Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys  
210 215 220

Thr Met Asp Ser His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr  
225 230 235 240

Gln Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly  
245 250 255

Leu Arg Cys Ser Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg  
260 265 270

Ala Pro Gly Thr Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys  
275 280 285

Asn Ser Met Lys Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro  
290 295 300

Thr Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu  
305 310 315 320

Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn  
325 330 335

Glu Glu Lys Met Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys  
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Ala Leu Lys Asn Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe  
355 360 365

Phe Pro Lys Val Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln  
370 375 380

Arg Lys Ala Leu Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser  
385 390 395 400

Val Asp Cys Ser Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg  
405 410 415

Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly  
420 425 430

Phe Tyr Met Ala Val Pro Ala Leu Ala Gly His Lys Lys Asp Ile Gly  
435 440 445

Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys  
450 455 460

Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg  
465 470 475 480

Val Phe Val Lys Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr  
485 490 495

Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly  
500 505 510

Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly  
515 520 525



Lys Thr Gly Glu Ile Ala Val Asp Gly Val Leu Leu Val Ser Gly Leu  
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Cys Pro Asp Ser Leu Leu Ser Val Asp Asp  
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<400> 31

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gcggcttagc tgctacgggg tccggccggc gccctcccga ggggggctca ggaggaggaa 240  
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Met Pro Leu Pro Trp Ser Leu Ala Leu Pro Leu  
1 5 10  
ctg ctc tcc tgg gtg gca ggt ggt ttc ggg aac gcg gcc agt gca agg 338  
Leu Leu Ser Trp Val Ala Gly Gly Phe Gly Asn Ala Ala Ser Ala Arg  
15 20 25  
cat cac ggg ttg tta gca tgc gca cgt cag cct ggg gtc tgt cac tat 386  
His His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly Val Cys His Tyr  
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Gly Thr Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys Gly  
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gtc tgt gaa gct aca tgc gaa cct gga tgt aag ttt ggt gag tgc gtg 482  
Val Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys Val  
60 65 70 75  
gga cca aac aaa tgc aga tgc ttt cca gga tac acc ggg aaa acc tgc 530  
Gly Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys  
80 85 90  
agt caa gat gtg aat gag tgt gga atg aaa ccc cgg cca tgc caa cac 578  
Ser Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His  
95 100 105  
aga tgt gtg aat aca cac gga agc tac aag tgc ttt tgc ctc agt ggc 626  
Arg Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly  
110 115 120  
cac atg ctc atg cca gat gct acg tgt gtg aac tct agg aca tgt gcc 674  
His Met Leu Met Pro Asp Ala Thr Cys Val Asn Ser Arg Thr Cys Ala  
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Met Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr Glu Glu Gly Pro Gln	
140 145 150 155	
tgc ctg tgt cca tcc tca gga ctc cgc ctg gcc cca aat gga aga gac	770
Cys Leu Cys Pro Ser Ser Gly Leu Arg Leu Ala Pro Asn Gly Arg Asp	
160 165 170	
tgt cta gat att gat gaa tgt gcc tct ggt aaa gtc atc tgt ccc tac	818
Cys Leu Asp Ile Asp Glu Cys Ala Ser Gly Lys Val Ile Cys Pro Tyr	
175 180 185	
aat cga aga tgt gtg aac aca ttt gga agc tac tac tgc aaa tgt cac	866
Asn Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys Cys His	
190 195 200	
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Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Tyr Asp Cys Ile Asp	
205 210 215	
ata aat gaa tgt act atg gat agc cat acg tgc agc cac cat gcc aat	962
Ile Asn Glu Cys Thr Met Asp Ser His Thr Cys Ser His His Ala Asn	
220 225 230 235	
tgc ttc aat acc caa ggg tcc ttc aag tgt aaa tgc aag cag gga tat	1010
Cys Phe Asn Thr Gln Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr	
240 245 250	
aaa ggc aat gga ctt cgg tgt tct gct atc cct gaa aat tct gtg aag	1058
Lys Gly Asn Gly Leu Arg Cys Ser Ala Ile Pro Glu Asn Ser Val Lys	
255 260 265	
gaa gtc ctc aga gca cct ggt acc atc aaa gac aga atc aag aag ttg	1106
Glu Val Leu Arg Ala Pro Gly Thr Ile Lys Asp Arg Ile Lys Lys Leu	
270 275 280	
ctt gct cac aaa aac agc atg aaa aag aag gca aaa att aaa aat gtt	1154
Leu Ala His Lys Asn Ser Met Lys Lys Lys Ala Lys Ile Lys Asn Val	
285 290 295	
acc cca gaa ccc acc agg act cct acc cct aag gtg aac ttg cag ccc	1202
Thr Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro	
300 305 310 315	
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Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly Gly	
320 325 330	
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Lys Lys Gly Asn Glu Glu Lys Met Lys Glu Gly Leu Glu Asp Glu Lys	
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Gly Asp Val Phe Phe Pro Lys Val Asn Glu Ala Gly Glu Phe Gly Leu	
365 370 375	

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Ile Leu Val Gln Arg Lys Ala Leu Thr Ser Lys Leu Glu His Lys Ala	
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Asp Leu Asn Ile Ser Val Asp Cys Ser Phe Asn His Gly Ile Cys Asp	
400 405 410	
tgg aaa cag gat aga gaa gat gat ttt gac tgg aat cct gct gat cga	1538
Trp Lys Gln Asp Arg Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp Arg	
415 420 425	
gat aat gct att ggc ttc tat atg gca gtt ccg gcc ttg gca ggt cac	1586
Asp Asn Ala Ile Gly Phe Tyr Met Ala Val Pro Ala Leu Ala Gly His	
430 435 440	
aag aaa gac att ggc cga ttg aaa ctt ctc cta cct gac ctg caa ccc	1634
Lys Lys Asp Ile Gly Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln Pro	
445 450 455	
caa agc aac ttc tgt ttg ctc ttt gat tac cgg ctg gcc gga gac aaa	1682
Gln Ser Asn Phe Cys Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp Lys	
460 465 470 475	
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Val Gly Lys Leu Arg Val Phe Val Lys Asn Ser Asn Asn Ala Leu Ala	
480 485 490	
tgg gag aag acc acg agt gag gat gaa aag tgg aag aca ggg aaa att	1778
Trp Glu Lys Thr Thr Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys Ile	
495 500 505	
cag ttg tat caa gga act gat gct acc aaa agc atc att ttt gaa gca	1826
Gln Leu Tyr Gln Gly Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu Ala	
510 515 520	
gaa cgt ggc aag ggc aaa acc ggc gaa atc gca gtg gat ggc gtc ttg	1874
Glu Arg Gly Lys Gly Lys Thr Gly Glu Ile Ala Val Asp Gly Val Leu	
525 530 535	
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Leu Val Ser Gly Leu Cys Pro Asp Ser Leu Leu Ser Val Asp Asp	
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<213> Homo sapiens

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Ala Ser Ala Arg Gln Pro Gly Val Cys His Tyr Gly Thr Lys Leu Ala  
35 40 45  
Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr  
50 55 60  
Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys  
65 70 75 80  
Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn  
85 90 95  
Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr  
100 105 110  
His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro  
115 120 125  
Asp Ala Thr Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln  
130 135 140  
Tyr Ser Cys Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser  
145 150 155 160  
Ser Gly Leu Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp  
165 170 175  
Glu Cys Ala Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val  
180 185 190  
Asn Thr Phe Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu  
195 200 205  
Gln Tyr Ile Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr  
210 215 220  
Met Asp Ser His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln  
225 230 235 240  
Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu  
245 250 255  
Arg Cys Ser Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala  
260 265 270  
Pro Gly Thr Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn  
275 280 285  
Ser Met Lys Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr  
290 295 300

Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu  
305 310 315 320

Ile Val Ser Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu  
325 330 335

Glu Lys Met Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala  
340 345 350

Leu Lys Asn Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe Phe  
355 360 365

Pro Lys Val Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg  
370 375 380

Lys Ala Leu Thr Ser Lys Leu Glu His Lys Ala Asp Leu Asn Ile Ser  
385 390 395 400

Val Asp Cys Ser Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg  
405 410 415

Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly  
420 425 430

Phe Tyr Met Ala Val Pro Ala Leu Ala Gly His Lys Lys Asp Ile Gly  
435 440 445

Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys  
450 455 460

Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg  
465 470 475 480

Val Phe Val Lys Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr  
485 490 495

Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly  
500 505 510

Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly  
515 520 525

Lys Thr Gly Glu Ile Ala Val Asp Gly Val Leu Leu Val Ser Gly Leu  
530 535 540

Cys Pro Asp Ser Leu Leu Ser Val Asp Asp  
545 550